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## SUMMARIES

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                                  The present invention describes a cross linked enzyme component (A), which (I) has an invented enzyme recondition site (RES) in a polypoptide of the component; and (ii) has at least one evalent intractable cross link between amino and sude elymbs of the polypoptide. The component tours an essymaticity active complex with a second orzyme the component due to the essymaticity active complex with a second orzyme.
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romplex prior to cleavage. The complex has eggymethe activity which is
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The present sequence represents a populae included in ligation
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CHAPT MAICH SIMILARITY TWO AS PROJECTION BY 20 LAMBET 104: Hest Local Similarity Two As Pred Ms. H. Se-19; Matches of Conservation of Ms. Marches of Debats of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               different from that of bota galactosidase. The component may be used for measurement of substances in biological samples, it is especially useful for measurement of enzymes (e.g. proteases, particularly viral, phosphatases, qycosidase, midase and esterase) in clinical samples, or for measurement, of target polypurchoolides. Assay methods using the new components exhibit extremely low inherent background signals, due to reduction or inhibition of complementation of enzyme components prior to cleavage. The present sequence represents a protein from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
75 caykttiqankhi Ivacequpytpvl.tdasv 104
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83 JUN 1999 (tirst entry)
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                                                         AAW99680 standard; inotein: 1 1 AA
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HIV; buman immunodeticlesey virus; cyclised prodrum; inhibition; covatently cross-linked; clearable site; suppression; inflammatory; immunological activity, area, cytotoxic effect.

Synthetic.

W09906072-A1

11-FEB-1999

24 - JUL - 1998; 98WO-78154 44

(BODE) BEDIRINGER MANNHEIM CLEP 40 - JUL - 1997; 970S-3054285

WP1: 1999 1676Je/14

New polypeptide prodrugs—chelude, e.g. an inserted enzyme recognition site and a covarent intrachain cross link between amino acid side chains of the polypeytide

Disclosure; Fig 6: 44pp: Fullish.

has an inserted enzyme reconsition site (ERS) in a polypoptide of the prodrug; and (ii) has at least one covalent intrachain cross-link between amino acid side claims of the polypoptide. The prodrug is converted to a therapositically more effective form upon cleavage of the ERS. (B) cross [inked prodrug; which; (i) has an inserted ERS in polypoptide of the prodrug; and (ii) has at least one cross linking morety (CLM) covalently builded between amino acid side chains of the polypeptide. The CLM comprises an enzymatically cleavable site. The product is convected to a therapout really more effective form upon cleavage of this site. The activated form of the product may have any desired belogical activity including activity in suppression of inflammatory or immuneledial activity, promotion of arowth or a direct cytoroxic effect on target series. Following cleavage of the ERS, the prodrug reassembles internable by unfolding or refolding, or reassembles The present invention describes: (A) cross-linked product, which: (i)

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The present invention describes a pair at parent plants for producing CC sequence encoding a polypoptide or protein A, and (b) a second parent of plant containing at least I gene sequence encoding a polypoptide or protein A, and (b) a second parent of plant containing at least I gene sequence encoding a polypoptide or cCC protein by whose the polypoptides A and by whom expressed it is exparate the polypoptides of a regularity protein or protein or protein containing the result of the same plant do form an active enzyme. The training the resultancy protein, or protein which afterts the structural interrity of a cell. Also described is a method for producing the first large protein and the second line where the containing protein a trist line with a second line where the containing protein a trist line with a second line where the containing polypoptide or more gene sequences encoding a polypoptide or protein a both which line does not have the desired phentype, the method comprising protein is complementary to the polypoptide or protein a both which line does not have the desired phentype. The method can be protein a bit in the polypoptide or protein a both the structural and the containing the polypoptide or protein and the polypoptide or protein a both the scanding a polypoptide or protein a both the scanding plants have the desired phentype. The method can be protein a protein and plants have the desired phentype. The method contains the contains and phentype the contains and plants have the desired phentype.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure: colum s il and 12: l'que
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composition of heronide resistance the
synthetic S(+5) protein which is used a
Sequence
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Query Mutch (V6. %) Best Lical Similarity (20. %) Matches 3:: Conservative

Score (1977) 28
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Sength 124:

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D. A. TALIHIA GASCINI, VALUHMIVOLI SAVO. 1

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MNAS protecto
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homologous relationship for the determination of mostly resembling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biological function with added a score on importance of expression of
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                 Region
                                                                           Chimeric
                                                                                            Chimeric
                                                                                                                                Spep-CBD Sprot; bovin
                                                                                                                                                  chimeric protein: S peptide cellulose binding domain-S protein;
                                                                                                                                                                                                       Polysaccharide modification: polysaccharide binding domain; PRD; paper;
                                                                                                                                                                                                                                             Chameric S peptide-cellulose binding domain-S protein.
                                                                                                                                                                                                                                                                                                                                                             AAE05749 standard: Protein:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein functions e.g. encoderic activity, for polypophides obtained from gene sequence 'runslation.
                                                                                                                                                                     wet strength: durability: classicity: cellulose bindina domain; CBD
                                                                                                                                                                                                                                                                                  24 SEP-2001 (first outry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           accurate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           medical context. The compaterised procedure is efficient, fast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are known. The database als econtains additional information on the score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid (aa) sequences of profess of which Lor more biological functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a database containing information on the amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the ENAS protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An efficient, accurate and rapid computer database for estimating
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                                                                       - Bos sp.
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"This region is derived from C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mise difference 327.328
              AAW:51.08.
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linking and/or multiples the properties of polysamchariae materials.
The method involves treating the polysamcharide structure with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparation of a polysorcharide containing material baying at least one destend structural, comball, physical, cleater at analyse mechanical
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                                                     AAW'5108 standard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   penetrate paper
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is S peptide-cellulose binding domain-S protein (Spep-CMD-Sprot), a lusion protein derived from Piostridium cellulovorans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which enhances the ability of the alkaline glue used in binding to
                                                                                                                                            297 Paykttqaakhii zaxxaapyxpyhidasx
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                                                                                                                            Cytotoxic: RNase; ribonelesse; pretes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             In immune and informmune diseases. Additionally, they may be used as east-convertices. Finally they can also be used to cell separation in retro-by sectority kuther unwanted types of cells (e.g. in know Marto-by) fined to transplantation into a patient underedding marrow about on by indiation of the Killing lenkemia cells of Localis that would consider all the seasons but discourse. This sequence represents a beginner panerrealist Phase A Lianment used to describe the method of the inzention.
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